

Microbiological Characteristics of *Chlamydia trachomatis* and *Neisseria gonorrhoeae* Infections in South African Women

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ABSTRACT

We analyzed data of 263 women with at least one genital or anorectal sexually transmitted infection from a cross-sectional study conducted in rural South Africa. We provide new insights concerning the concurrence of *Chlamydia trachomatis*, *Neisseria gonorrhoeae*, *Mycoplasma genitalium*, and *Trichomonas vaginalis* infections as well as the characteristics of bacterial loads.

TEXT

Chlamydia trachomatis and *Neisseria gonorrhoeae* are the most prevalent bacterial sexually transmitted infections (STI) in the world (1). The course of these infections is unpredictable and diverse (2–7). Most infections in women are asymptomatic and frequently remain unrecognized, which increases the risk for reproductive tract complications (6, 8–10). Insight into the mechanisms that drive the burden of these infections is essential for disease control. In addition to age, HIV infection, and behavioral factors, microbiological characteristics, including bacterial load, may play an important role in the risk of transmission, clinical presentation, and course of infection (6, 11–14). Chlamydial load has been associated with clinical presentation, severity of infection, and transmissibility in animal models and in patients with ocular *C. trachomatis* infection (15–17). Gonorrheal loads have been shown to differ between anatomic locations and associated clinical presentations in men (18). Although real-time PCR and quantitation of DNA load have the potential of revealing new insights into the characteristics of infection, there is only limited literature about the relevance of bacterial load and frequency of concurrent STI in women (19, 20). Knowledge about microbiological characteristics of infection could possibly help to improve understanding of the differences in STI prevalences at the population level. This

study aimed to evaluate the concurrence and bacterial loads of genital and anorectal *C. trachomatis* and *N. gonorrhoeae* infections in South African women from a setting of high HIV prevalence.

This study was a subanalysis of a previously described cross-sectional study of 604 women in rural Mopani District, South Africa (21). In brief, consenting women 18 to 49 years of age who reported sexual activity during the previous 6 months were eligible. Questionnaires were completed and vaginal, anorectal and pharyngeal swabs (Copan Diagnostics, Brescia, Italy) were obtained by health care workers and stored at -20°C . Menses on the day of recruitment and refusal to have all three anatomic sites tested were exclusion criteria. Symptomatic women were treated the same day according to local treatment protocols, which include a notification slip for the partner. Asymptomatic women with an STI proven by molecular detection were called to return to the clinic for specific treatment. For the evaluation presented in this article, we selected all women ($n = 263$) vaginally and/or anorectally infected with at least one of the following pathogens: *C. trachomatis* ($n = 107$), *N. gonorrhoeae* ($n = 66$), *Mycoplasma genitalium* ($n = 66$), and *Trichomonas vaginalis* ($n = 116$). As we observed only one woman with an oropharyngeal infection, we excluded this anatomical location from further analyses. The Human Ethics Research Committee of the University of the Witwatersrand, South Africa, approved the study (reference no. M110726), including the *M. genitalium* and *T. vaginalis* testing.

Dry swabs were transported on dry ice in order to perform laboratory analysis at the Laboratory of Immunogenetics, VU University Medical Center, Amsterdam, the Netherlands. Bacterial DNA was extracted using a High Pure PCR template preparation kit (Roche Diagnostics, Indianapolis, IN) followed by real-time PCR detection of *C. trachomatis*, *N. gonorrhoeae*, and *T. vaginalis* using a PrestoPluS CT-NG-TV assay (Microbiome Ltd., Amsterdam, the Netherlands) and a LightMix real-time PCR kit (TIB Molbiol, Berlin, Germany) for *M. genitalium* as described elsewhere (21, 22) (D. J. de Waaij, J. H. Dubbink, R. P. H. Peters, S. Ouburg, and S.A. Morré, unpublished data). The bacterial DNA load of *C. trachomatis* and *N. gonorrhoeae* was calculated as follows. The C_p (crossing-point) value, i.e., the number of amplification cycles before a standardized threshold is reached, was related to a calibration curve of a known *C. trachomatis* DNA quantity and *N. gonorrhoeae* DNA quantity to determine the amount of bacterial DNA. In our analysis, the bacterial load is provided as the logarithm of the number of inclusion-forming units (IFU) per nanoliter for *C. trachomatis* and as the logarithm of the number of copies per microliter for *N. gonorrhoeae*. Statistical analyses were performed using the chi-square test or Fisher's exact test and Mann-Whitney U test to compare dichotomous and continuous variables between groups. A P value of less than 0.05 was considered statistically significant for all tests.

Of the 263 women with a genital and/or anorectal STI, 247 (94%) had a genital STI and 73 (27%) an anorectal STI. The median age of all women ($n = 263$) was 29 (range, 18 to 49) years and HIV infection was reported by 33%, whereas 44% reported testing HIV negative in the last 6 months and 24% did not know their status. Fellatio was reported by 13% of the women and receptive anal intercourse (RAI) by 5.5%.

The distribution of genital microorganisms is shown in Fig. 1. Anorectal infection was caused in 64 (88%)/73 women by a single microorganism: *C. trachomatis* in 34/43, *N. gonorrhoeae*

in 9/15, *M. genitalium* in 16/17, and *T. vaginalis* in 5/7. Single infections were significantly more common at the anorectal than at the genital location (88% versus 74%, $P = 0.013$). Among the 107 women with a *C. trachomatis* infection, 32 (30%) women had a double infection (combined genital and rectal infection). Among the 66 women with a *N. gonorrhoeae* infection, 9 (14%) women had a double infection. Within the 66 and 116 women with a *M. genitalium* infection and a *T. vaginalis* infection, 3 (4.5%) and 4 (3.4%) women had a double infection, respectively.

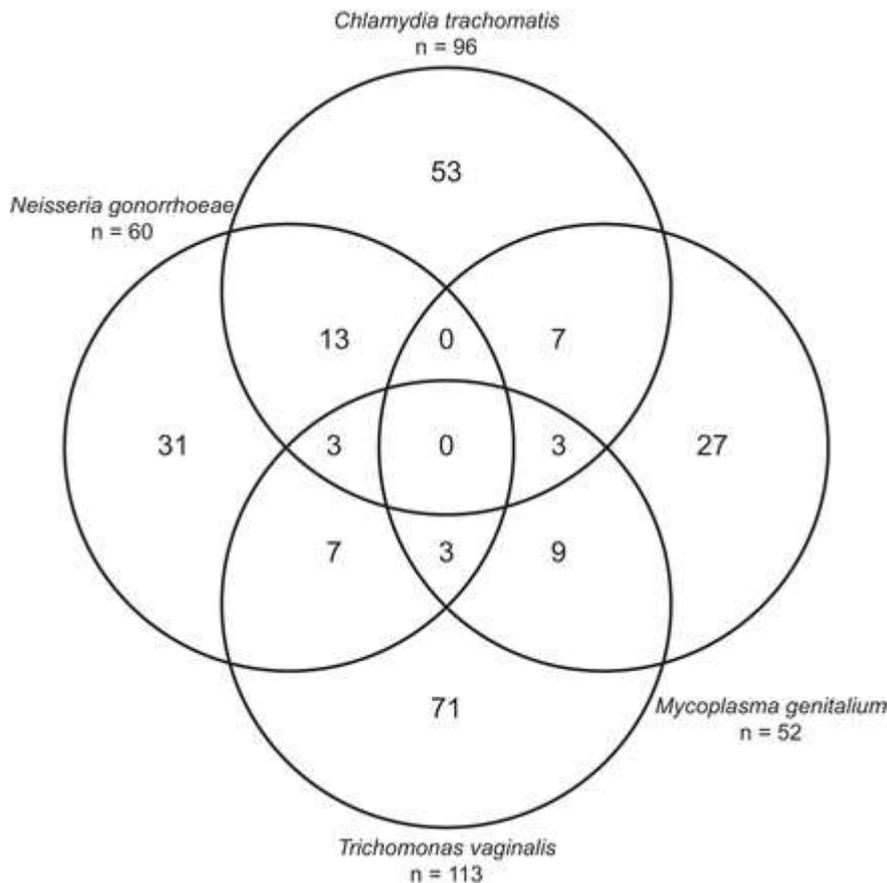


FIG 1. Venn diagram of multiple genital infections. Note that the double infections of *Chlamydia trachomatis* with *Trichomonas vaginalis* ($n = 17$) and *Neisseria gonorrhoeae* with *Mycoplasma genitalium* ($n = 3$) are not represented in the figure. The number of infections in each circle equals the total amount (n) given.

The median load of genital *C. trachomatis* was $2.7 \log_{10}$ IFU/nl (range, 0.36 to 4.5), and that of anorectal *C. trachomatis* was $2.5 \log_{10}$ IFU/nl (range, 0.58 to 3.6). For *N. gonorrhoeae*, the median load of genital infection was $2.7 \log_{10}$ copies/ μ l (range, 1.6 to 8.0) and that of rectal infection was $4.4 \log_{10}$ copies/ μ l (range, 2.2 to 6.3). Characteristics and associations of genital and rectal bacterial load are presented in Table 1. In multivariate analyses, age of ≤ 24 years ($P = 0.009$) and pregnancy ($P = 0.023$) were independently associated with a higher *C. trachomatis* load and same age group ($P < 0.0001$) and having had more than 1 sexual partner in last 6 months ($P = 0.029$) with a higher *N. gonorrhoeae* load. The association of a concurrent relationship in the last year with *N. gonorrhoeae* load was no longer manifest in multivariate analysis ($P = 0.32$).

TABLE 1 Characteristics of and associations with bacterial load^a

Patient category	<i>Chlamydia trachomatis</i>		<i>Neisseria gonorrhoeae</i>	
	Median log ₁₀ IFU/nl	<i>P</i>	Median log ₁₀ copies/μl	<i>P</i>
Characteristics of genital bacterial load				
Single genital infection	2.7		2.9	
Mixed genital infection with ^b :				
<i>Chlamydia trachomatis</i>			2.6	0.55
<i>Neisseria gonorrhoeae</i>	1.6	0.06		
<i>Mycoplasma genitalium</i>	2.9	0.60	3.1	0.23
<i>Trichomonas vaginalis</i>	2.7	0.70	3.6	0.16
Reported HIV infection ^c				
Yes	2.6	0.52	2.5	0.56
No	2.7		3.0	
Genital infection status ^d				
Symptomatic	2.6	0.54	3.3	0.16
Asymptomatic	2.7		2.7	
Infection category				
Single (genital only)	2.3	0.002	2.7	0.004
Double	3.2		5.8	
Characteristics of rectal bacterial load				
Infection category				
Single (anorectal only)	2.7	0.63	4.0	0.39
Double	2.1		4.9	
Associations with genital bacterial load				
Age				
≤24 yrs	3.0	0.010	5.5	<0.001
>24 yrs	2.5		2.5	
Currently pregnant				
Yes	3.4	0.017	3.0	0.29
No	2.5		2.5	
Hormonal injections				
Yes	2.7	0.96	3.0	0.45
No	2.6		2.7	
Intravaginal cleansing				
Yes	3.0	0.29	2.5	0.11
No	2.7		3.0	
No. of sexual partners in last 6 mo				
≤1 partner	2.7	0.66	2.7	0.028
>1 partners	3.0		5.2	
Days since last sex act				
≤7 days	2.7	0.70	2.7	0.61
>7 days	2.5		2.9	
Concurrent relationship <1 yr earlier				
Yes	2.7	0.58	4.9	0.021
No	2.7		2.6	

^a Boldface data indicate statistically significant results.

^b Mixed infection per pathogen given, with the *P* value related to single-infection data as a reference.

^c HIV (human immunodeficiency virus), HIV-positive status compared with negative status in the previous 6 months.

^d Genital infection is defined as symptomatic when abnormal vaginal discharge, intramenstrual bleeding, or vaginal blood loss during or after sexual intercourse was reported.

This report describes the concurrence of STI and bacterial DNA load in South African women with genital and anorectal *Chlamydia trachomatis* and *Neisseria gonorrhoeae* infection. Only a few reports of studies on these microbiological characteristics of infection have been published, and to our knowledge, this is the first report of a study conducted in a rural setting of high HIV prevalence. We observed that nearly half of the women with genital *C. trachomatis* infection (47%) and *N. gonorrhoeae* infection (48%) had a concomitant genital infection. Although there is limited knowledge about the significance of mixed infections, these might theoretically increase susceptibility to long-term complications and transmissibility for individual STI. Mixed rectal infections were significantly less common among women than genital STI, as 88% of these infections were caused by a single microorganism. Potential explanations would be less-frequent exposure to infection, as RAI was not common in our cohort, and different susceptibilities of the anorectal mucosa for certain microorganisms.

Women with a double infection had significantly higher *C. trachomatis* and *N. gonorrhoeae* genital loads than women with genital infection only. To our knowledge, this has not been reported before and might support the hypothesis of autoinoculation through cervicovaginal fluids from the vagina to the rectum. This possible role of spillover might explain the high prevalence of anorectal infection despite the low frequency of RAI in our study (23, 24).

We observed no significant difference between the bacterial loads of single and mixed infections for any of the STI. In line with two other nucleic acid amplification test (NAAT)-based studies, we did not observe a relation between bacterial load and genital symptomatology (25, 26). Vodstrcil and colleagues observed in a recent review that culture-based studies are more likely to find an association with signs and symptoms than NAAT-based studies (89% versus 38%) (27). This might be reflected by the tendency of viable organisms to be more closely associated with clinical manifestations. Younger age and pregnancy were independently associated with a higher bacterial load of *C. trachomatis* and younger age and having had more than one sexual partner in the last 6 months with a higher load of *N. gonorrhoeae*. The same relation with age (for *C. trachomatis*) in several NAAT studies has been described before and might be due to changes in the cervical epithelium or to younger women being more sexually active and exhibiting riskier behavior or might reflect acquired immunity in adults (28–30). There were several limitations to our study. First, we did not account for sampling variability by reporting loads corresponding to the number of eukaryotic cells. However, as inflammatory cells which are attracted to the site of infection would be included among the sampled cells, the load per eukaryotic cell would be decreased (25). A second limitation may be the use of stored specimens, but the literature does not show a clinically relevant degradation impact (31). A last limitation may be represented by women using antimicrobials, a factor which might have caused us to underestimate our results to some extent, as this was not an exclusion criterion.

In conclusion, this study revealed frequent concurrent infections of *C. trachomatis* and *N. gonorrhoeae* and differences in bacterial loads in a setting of high HIV prevalence. These new insights might help to explain differences in STI prevalence at a population level where increased efforts are needed to control the burden of *C. trachomatis* and *N. gonorrhoeae* infections.

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The rest of us declare that we have no potential conflicts of interest.

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